

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising:
 - 5 (a) a nucleotide sequence encoding a polypeptide required for proper root formation, wherein the polypeptide has an amino acid sequence of at least 70% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, 8, 30, or 38; or
 - (b) a complement of the nucleotide sequence, wherein the complement
10 and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary.
2. The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 75% sequence identity, based on the Clustal V method
15 of alignment, when compared to one of SEQ ID NO:6, 8,30, or 38.
3. The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 80% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, 8 ,30, or 38.
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4. The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 85% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, 8 ,30, or 38.
- 25 5. The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 90% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, 8 ,30, or 38.
6. The polynucleotide of Claim 1, wherein the amino acid sequence of
30 the polypeptide has at least 95% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, 8 ,30, or 38.
7. The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 99% sequence identity, based on the Clustal V method
35 of alignment, when compared to SEQ ID NO: 6, 8 ,30, or 38.

8. The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide comprises one of SEQ ID NO:6, 8, 30, or 38.

9. The polynucleotide of Claim 1 wherein the nucleotide sequence
5 comprises one of SEQ ID NO:5, 7, 29 or 37.

10. The isolated polynucleotide of Claim 1, wherein the nucleotide sequence comprises at least two motifs selected from group consisting of SEQ ID NOs:9, 10, 11, 12 and 13, wherein said motif is a substantially conserved
10 subsequence.

11. A functionally equivalent subfragment of the isolated polynucleotide of Claim 1, wherein said subfragment is useful in antisense inhibition or co-suppression of expression of a nucleic acid sequence encoding the polypeptide of
15 Claim 1.

12. An isolated nucleic acid fragment comprising a promoter consisting essentially of SEQ ID NO:2, 3 or 4, or a substantially similar and functionally equivalent subfragment of said promoter.
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13. A recombinant DNA construct comprising the isolated polynucleotide of Claim 1 or a functionally equivalent subfragment thereof, operably linked to at least one regulatory sequence.

14. The recombinant DNA construct of Claim 13, wherein said at least one regulatory sequence comprises the promoter of Claim 12.
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15. A plant comprising in its genome the recombinant DNA construct of Claim 13.
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16. A seed obtained from the plant of Claim 15.

17. The plant of Claim 15, wherein said plant is selected from the group consisting of rice, corn, sorghum, millet, rye, soybean, canola, wheat, barley, oat,
35 beans, and nuts.

18. Transformed plant tissue or plant cell comprising the recombinant DNA construct of Claim 13.

19. A method of altering root structure during plant development, comprising:

- (a) transforming a plant with the recombinant DNA construct of Claim 13;
- (b) growing the transformed plant under conditions suitable for the expression of the recombinant DNA construct; and
- (c) selecting those transformed plants having altered root structure.

20. A method to isolate nucleic acid fragments encoding polypeptides associated with altering root structure during plant development, comprising:

- (a) comparing SEQ ID NOs:6,8 30, or 38 with other polypeptide sequences associated with altering root structure during plant development;
- (b) identifying the conserved sequences(s) or 4 or more amino acids obtained in step (a);
- (c) making region-specific nucleotide probe(s) or oligomer(s) based on the conserved sequences identified in step (b); and
- (d) using the nucleotide probe(s) or oligomer(s) of step (c) to isolate sequences associated with altering root structure during plant development by sequence dependent protocols.

21. A method of mapping genetic variations related to altering root structure in plants comprising:

- (a) crossing two plant varieties; and
 - (b) evaluating genetic variations with respect to:
 - (i) a nucleic acid sequence selected from the group consisting of SEQ ID NO:1,2,3,4,5,7, 28, 29, or 37; or
 - (ii) a nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NO:6, 8 , 30, or 38;
- in progeny plants resulting from the cross of step (a), wherein the evaluation is made using a method selected from the group consisting of: RFLP analysis, SNP analysis, and PCR-based analysis.

22. A method of molecular breeding to alter root structure during plant development in plants comprising:

- (a) crossing two plant varieties; and
- (b) evaluating genetic variations with respect to:
 - (i) a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, 2,3,4,5, 7, 28, 29, or 37; or

(ii) a nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NO:6, 8, 30, or 38;
in progeny plants resulting from the cross of step (a), wherein the evaluation is made using a method selected from the group consisting of: RFLP analysis, SNP analysis, and PCR-based analysis.